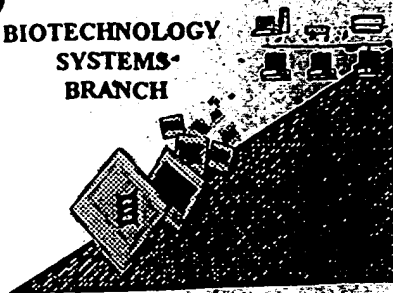


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/915706
Source: OIFE
Date Processed by STIC: 10/17/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/915706

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 3rd amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length.
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequence:
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represent
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rule
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/915,706

DATE: 10/17/2001
TIME: 15:54:53

Input Set : A:\5112.app
Output Set: N:\CRF3\10172001\I915706.raw

3 <110> APPLICANT: NELSON, DAVID R.
5 <120> TITLE OF INVENTION: A LIVE, AVIRULENT STRAIN OF V. ANGUILLARUM THAT
6 PROTECTS FISH AGAINST INFECTION BY VIRULENT V.
7 ANGUILLARUM
9 <130> FILE REFERENCE: 5112
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/915,706 *OK*
C--> 12 <141> CURRENT FILING DATE: 2001-07-26 *OK*
14 <160> NUMBER OF SEQ ID NOS: 4
16 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
Corrected Sequence Needed

ERRORED SEQUENCES

See page 2 of 4

18 <210> SEQ ID NO: 1
19 <211> LENGTH: 3609
20 <212> TYPE: DNA
21 <213> ORGANISM: V. Anguillarum
23 <220> FEATURE:
24 <223> OTHER INFORMATION: "n" bases may be a, t, c, g, other or unknown
26 <400> SEQUENCE: 1
27 gtcgacttat tgcattgatg gcgtacatgg tagtgccatc cttcgtttgc taacaagcgt 60
28 tgtataaaag cttggtcggt ttcacatcaagt tgaacacaat actcatgatt tttcccactt 120
29 ccggaagagg aaaagtgaat atagcttttg agatcagcct gttctagcag cttttcaatg 180
30 atcttttttcg tcgttacggt ttgaaaaatc tgacgactgc gtttgtattg caacaagcta 240
31 agtggatcca atatctctat ttgataataa aactgctgct tgcctttgct atatcctgtg 300
32 aattgcagag tgctacatat acctgaaaaa aaacgctttc cagaatctaa ttcgtaagac 360
33 acacaaacag ctttacctag gtttttggtg tcgatctcca tgtttgccgc gatggaaacg 420
34 gaaaactgac acccgccgga tacgctttcc tctccgatta attgcgtgac aatataactt 480
35 ttgctatctg aaagcttaat ggtgaggagg cgggtttggt gctttaattc gttactgctc 540
36 atattcaatt aattcactat taaataaaca gttctaaaag gctgtttatt ggatgaatat 600
37 tcgaaattat cacataataa ttgatgctat tattacttgc tgtattggtg tcaactttca 660
38 tgctctatac atgtaataa tttcgagtta gaccttaatt caaggttaatt tgtctattta 720
39 attattatct gaataatatg taatcgattg ctttgtggtt atttttatgt ttgtttcatt 780
40 tttaatgacg gtgagcttgt gcattcatat tttttatgat gacaacatct ttgatgaagt 840
41 atttaagata ttgttaatgc atgagggggt tgcgtgtatt ttttatatta aatcataata 900
42 aaatcaacaa tatatgttat tttgtgtcct tttatagtgt tcttttaaaag aggtaggatg 960
43 acctaaaggt cgcctagaaa tatggcgtaa attgccattg ctataattca cctcaaagat 1020
44 acactattgg caaattgaca aatatgtcac ttcgtatgaa acaatattag tagatgttgt 1080
45 ttttgctgca aaaataaaaa ttttctggtg tgaaataact caaggcctct agcgttttcc 1140
46 tttatcttaa aatacaggaa atagcgattg aagttaattg acacttaagc aasdramgaa 1200
47 tagtcaacct aacagagcag gaacctatgc ctttgtcaaa gcatcaaatt gagcaacttt 1260
48 ctaaacctct gagtgatgat tcgatctgtg gcgtttatct taaactggaa aaaagtgcct 1320
49 ttcgcccatt acgtaatgaa tttaatgtcg cgcaaaactgc gctgcgtaag ctaagtcaaa 1380
50 accctagtgc tgacgagaga gatgcgttac aagaggcatg tctaaataag tggaagattc 1440
51 tctctgacag tttgtacgaa cagttttcaa aaacaaccag agatatcgag ctcatctcat 1500
52 ggtttgttgc tgctcaattc cttctcgata ccacattaga aagtgtctgc aatagccttg 1560
53 agtggttagc ggatttaagt gagaagcact gggatcacct caaccctgta ctaccagttg 1620

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/915,706

DATE: 10/17/2001

TIME: 15:54:53

Input Set : A:\5112.app

Output Set: N:\CRF3\10172001\I915706.raw

54 aaacgctcaa atctgatgat gataagggca aagaaagaga gcaagcagat gcgaaagtta 1680
 55 aagcattttt ccaactagtc ggcgatagcg aggaaagctc gattctctat gcgcccgtgc 1740
 56 tgcaactgcc cttagtcggg gaagtgacgt tttttgactt tcaaagtgc gagagaaaag 1800
 57 gogaaatcag ccaactgaaa tctatgctta cgaccacggg ggcgcaagag cgtttcgcaa 1860
 58 ttcaattcaa gatggaaaac gccaaacggt gtgtcaccca attagatcgt ttgtcagcgt 1920
 59 tgggtgagcac taagtgtcat tctctaggca gtcaaagtac caacttcgga tttgcgaagt 1980
 60 cactgcttac ccgtgttgaa aacgctttgg ttcacttaag tggaaattaag ttagcaccga 2040
 61 aagcggaggc caagacagta gagcaagagg ttgccgaaag ttcagtttct gaaggggagc 2100
 62 tgccaagcca tatggataca aaacatatag agcgaatacc gatggcatca gagcaggctc 2160
 63 agaccgtaag ccaacactta cagcgaggaa acctctctga actgggtaat ttaaacaata 2220
 64 tgaaccgaga cttagctttc catttggtga gagaagtctc tgattatttt cgccagagcg 2280
 65 aaccgcatag cccaatttca tttttgttag aaaaagcgat tcgatgggga tatttatect 2340
 66 tacctgagtt gctgcgagaa atgatgtcgg aacaaaacgg tgacgctctt agtacgattt 2400
 67 ttaatgccgc cggattgaat catctcgatc aggttttgcg gccggagggt agtactccaa 2460
 68 cgggtgggcat tgaaagcccc caaacacctc aagcgaagcc ttccgtttcg gatccgcgaa 2520
 69 gtgttgaaaga gcatgtatct cagacttccc ctgtagatac ccaatctaag caagatcaaa 2580
 E--> 70 aaccacaatc atccgcta* drbcgtcggc tctgagttgg taattgtggt taaaaaataa 2640
 71 ggaaaaatca tggcaagtat ttacatgcgt gtaagcggtc ttcaagttga gggcgagcg 2700
 72 actatcggtc agctagaaac ggctgaaggt aaaaatgacg gttggtttgc aatcaactct 2760
 73 tactcttggg gtggcgctcg taacgttgct atggacatcg gtaacggcac caatgcggat 2820
 74 tcaggcatgg ttggcgtaag cgaagttagc gtaactaaag aagtcgatgg tgcttctgaa 2880
 75 gacctactgt cttatttatt caaccaggt aaagacggta aaactgttga ggttgcatth 2940
 76 actaagcctt ctaacgatgg tcaaggtgca gacgtttact tccaagttaa gctagaaaaa 3000
 77 gcacgtttag tttcttaca cgtgagcggg actgacggat ctcaaccgta cgagagccta 3060
 78 tctctttctt acacttctat ttctcagaag catcactatg agaaagaagg tggtaacta 3120
 E--> 79 caaagcgggt gtgttgtgac ttacgacctc ccgaccggga aaatgactt ctggtaagta 3180
 80 attctttcat tagacatgcc acgttaattg gcatgtctat ttcatgaata tctcsdrcat 3240
 81 tttaggacac cgttatggca ttgaactcac aacataagcg cgtagtaag aaccgtgtca 3300
 82 gcatcaccta tgacgttgaa acgaatggcg ccgtaaagac gaaagagctg ccgtttgttg 3360
 83 ttggcgctcat tggcgacttt tcaggacaca aaccagaatc agaaaaagtt gatttagaag 3420
 84 agcgagagtt cacgggtatc gataaagaca acttcgatac agtgatggg caaattcacc 3480
 85 cgcgtctttc gtacaaggtt gataacaagc ttgctaata gaatagccag tttgaagtga 3540
 W--> 86 acttgagcct ccgttcgatg aaagatttcc acccagagaa cttagttgat naaattgagc 3600
 87 cgcttaaa 3609

Stop codons
are not acceptable
in non-coding
sequences.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

specifically
Sequence 4.

Sequence 1 Errors:
n's must be enumerated
in fields 221, 222 and
223.

1. Field 221 must be "unclear"
2. Field 222 must be a location
in the sequence
3. Field 223 must be a n =
some string of possible
unknowns

VERIFICATION SUMMARY

DATE: 10/17/2001

PATENT APPLICATION: US/09/915,706

TIME: 15:54:54

Input Set : A:\5112.app

Output Set: N:\CRF3\10172001\I915706.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:70 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:79 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:86 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:86 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:86 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:253 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:253 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

<400> 4

Met Ala Leu Asn Ser Gln His Lys Arg Val Ser Lys Asn Arg Val Ser
 1 5 10 15

Ile Thr Tyr Asp Val Glu Thr Asn Gly Ala Val Lys Thr Lys Glu Leu
 20 25 30

Pro Phe Val Val Gly Val Ile Gly Asp Phe Ser Gly His Lys Pro Glu
 35 40 45

Ser Glu Lys Val Asp Leu Glu Glu Arg Glu Phe Thr Gly Ile Asp Lys
 50 55 60

Asp Asn Phe Asp Thr Val Met Gly Gln Ile His Pro Arg Leu Ser Tyr
 65 70 75 80

Lys Val Asp Asn Lys Leu Ala Asn Asp Asp Ser Gln Phe Glu Val Asn
 85 90 95

Leu Ser Leu Arg Ser Met Lys Asp Phe His Pro Glu Asn Leu Val Asp
 100 105 110

Xaa Ile Glu Pro Leu
 115